

SEQUENCE LISTING OS TASAKA, MASAO FUKAKI, HIDEHIRO A PROTEIN THAT HAS A FUNCTION OF MAINTAINING A MUTATION WHEREBY <120> LATERAL ROOT FORMATION IS BLOCKED AND A GENE ENCODING THE PROTEIN <130> 245787US0 <140> 10/718,513 <141> 2003-11-24 JP 2003-147765 2003-05-26 <150> <151> <160> 32 <170> PatentIn version 3.2 <210> 4155 <211> <212> DNA Arabidopsis thaliana <220> <221> **CDS** (1)..(4152) <400> atg agt agt ttg gtg gag agg ctt cgc ata cga tct gat agg aaa cca Met Ser Ser Leu Val Glu Arg Leu Arg Ile Arg Ser Asp Arg Lys Pro 48 gtt tat aac cta gat gat tct gat gat gac gac ttc gtt cct aaa aaa Val Tyr Asn Leu Asp Asp Ser Asp Asp Asp Asp Phe Val Pro Lys Lys 20 25 3096 gat cga acc ttt gag caa gtc gag gct att gtc aga act gat gcg aaa Asp Arg Thr Phe Glu Gln Val Glu Ala Ile Val Arg Thr Asp Ala Lys 144 gaa aat gca tgt cag gct tgt ggg gaa agt act aat ctt gta agc tgc Glu Asn Ala Cys Gln Ala Cys Gly Glu Ser Thr Asn Leu Val Ser Cys 50 55 60 192 aat aca tgc act tat gcg ttc cat gct aaa tgc tta gtt cca cct ctt Asn Thr Cys Thr Tyr Ala Phe His Ala Lys Cys Leu Val Pro Pro Leu 65 70 75 80 240 aaa gat gct tcc gtg gaa aat tgg aga tgc cct gaa tgt gtt agt cct Lys Asp Ala Ser Val Glu Asn Trp Arg Cys Pro Glu Cys Val Ser Pro 85 90 95 288 ctt aac gag ata gat aag ata ttg gat tgt gaa atg cgt cct aca aaa Leu Asn Glu Ile Asp Lys Ile Leu Asp Cys Glu Met Arg Pro Thr Lys 100 105 110336 tct agt gaa caa ggt tcc tcc gat gcg gaa ccg aag cca att ttt gtg Ser Ser Glu Gln Gly Ser Ser Asp Ala Glu Pro Lys Pro Ile Phe Val 115 120 125 384 432

tgg gtg cct gag aag gag ttc cag aag gct tat aag tca aat cat cgt Trp Val Pro Glu Lys Glu Phe Gln Lys Ala Tyr Lys Ser Asn His Arg 480

145					150					155					160	
tta Leu	aaa Lys	acc Thr	aga Arg	gtg Val 165	aac Asn	aat Asn	ttt Phe	cac His	cgt Arg 170	caa Gln	atg Met	gag Glu	tca Ser	ttc Phe 175	aat Asn	528
aac Asn	agc Ser	gaa Glu	gat Asp 180	gat Asp	ttt Phe	gtt Val	gcc Ala	ata Ile 185	cgt Arg	cct Pro	gag Glu	tgg Trp	acc Thr 190	act Thr	gtt Val	576
gat Asp	cgg Arg	att Ile 195	ctt Leu	gcc Ala	tgc Cys	aga Arg	gag Glu 200	gaa Glu	gat Asp	ggg Gly	gag Glu	ctg Leu 205	gaa Glu	tat Tyr	ctt Leu	624
gtc Val	aaa Lys 210	tat Tyr	aaa Lys	gag Glu	cta Leu	tcc Ser 215	tat Tyr	gat Asp	gaa Glu	tgt Cys	tat Tyr 220	tgg Trp	gag Glu	tca Ser	gaa Glu	672
tca Ser 225	gac Asp	atc Ile	tca Ser	acc Thr	ttc Phe 230	cag Gln	aat Asn	gaa Glu	att Ile	caa Gln 235	agg Arg	ttc Phe	aag Lys	gat Asp	gta Val 240	720
aat Asn	tct Ser	aga Arg	act Thr	cgc Arg 245	aga Arg	agt Ser	aaa Lys	gat Asp	gtt Val 250	gac Asp	cat His	aaa Lys	aga Arg	aat Asn 255	CCC Pro	768
aga Arg	gac Asp	ttt Phe	caa Gln 260	cag Gln	ttt Phe	gat Asp	cat His	act Thr 265	cct Pro	gaa Glu	ttc Phe	ctc Leu	aaa Lys 270	ggc Gly	ttg Leu	816
tta Leu	cat His	cca Pro 275	tac Tyr	cag Gln	ctt Leu	gag Glu	gga Gly 280	ctt Leu	aat Asn	ttt Phe	ttg Leu	cgg Arg 285	ttc Phe	tcg Ser	tgg Trp	864
tca Ser	aaa Lys 290	cag Gln	acg Thr	cat His	gta Val	atc Ile 295	ctt Leu	gct Ala	gat Asp	gaa Glu	atg Met 300	gga Gly	cta Leu	ggc Gly	aag Lys	912
aca Thr 305	att Ile	caa Gln	agc Ser	att Ile	gcc Ala 310	ctt Leu	tta Leu	gct Ala	tca Ser	ctt Leu 315	ttt Phe	gag Glu	gag Glu	aac Asn	ctc Leu 320	960
								cta Leu								1008
aga Arg	gag Glu	ttt Phe	gcc Ala 340	Thr	tgg Trp	gcc Ala	cca Pro	cag Gln 345	atg Met	aac Asn	gtg Val	gtt Val	atg Met 350	Tyr	ttt Phe	1056
ggc Gly	act Thr	gcg Ala 355	caa Gln	gct Ala	cga Arg	gca Ala	gtt Val 360	Ile	aga Arg	gaa Glu	cat His	gag Glu 365	ttt Phe	tac Tyr	tta Leu	1104
		Āsp										Gly			agt Ser	1152
						Arg									tcg Ser 400	1200
					Leu					Leu					tgg Trp	1248
gag Glu	tgc Cys	atg Met	att Ile 420	٧a٦	gat Asp	gaa Glu	ggt Gly	cat His 425	Arg	ctg Leu 2	aaa Lys	aat Asn	aag Lys 430	Asp	tca Ser	1296

aag Lys	ctg Leu	ttc Phe 435	tct Ser	tca Ser	ttg Leu	aca Thr	cag Gln 440	tat Tyr	tca Ser	agt Ser	aac Asn	cac His 445	cgt Arg	att Ile	ctt Leu	1	344
ctg Leu	aca Thr 450	gga Gly	aca Thr	cca Pro	ctt Leu	cag Gln 455	aac Asn	aac Asn	ttg Leu	gat Asp	gaa Glu 460	ctt Leu	ttc Phe	atg Met	ctc Leu	1	392
atg Met 465	cat His	ttt Phe	ctt Leu	gat Asp	gcg Ala 470	ggg Gly	aag Lys	ttt Phe	gga Gly	agt Ser 475	ttg Leu	gag Glu	gag Glu	ttc Phe	cag Gln 480	1	440
gag Glu	gag Glu	ttc Phe	aaa Lys	gat Asp 485	att Ile	aat Asn	caa Gln.	gag Glu	gag Glu 490	cag Gln	atc Ile	tca Ser	agg Arg	ttg Leu 495	сас His	1	488
								aga Arg 505								1	536
aaa Lys	gac Asp	atg Met 515	ccc Pro	ccc Pro	aaa Lys	aag Lys	gag Glu 520	ctc Leu	att Ile	ttg Leu	cgt Arg	gtt Val 525	gat Asp	ctg Leu	agc Ser	1	584
								gct Ala								1	632
gta Val 545	ttg Leu	aca Thr	aaa Lys	aag Lys	gga Gly 550	ggt Gly	gct Ala	caa Gln	att Ile	tcc ser 555	ctt Leu	aat Asn	aac Asn	att Ile	atg Met 560	1	680
								cat His								1	728
gag Glu	cca Pro	gtt Val	att Ile 580	cac His	gac Asp	gca Ala	aat Asn	gaa Glu 585	gct Ala	ttc Phe	aaa Lys	caa Gln	ctt Leu 590	ttg Leu	gag Glu	1	776
tct Ser	tgt Cys	gga Gly 595	aag Lys	ctg Leu	caa Gln	ctt Leu	cta Leu 600	gat Asp	aaa Lys	atg Met	atg Met	gtc Val 605	aaa Lys	ctg Leu	aaa Lys	1	824
gag Glu	caa Gln 610	gga Gly	cac His	aga Arg	gtc Val	cta Leu 615	ata Ile	tac Tyr	aca Thr	cag Gln	ttt Phe 620	cag Gln	cat His	atg Met	ctg Leu	1	872
						Cys		cat His								1	920
att Ile	gat Asp	gga Gly	aag Lys	gtt Val 645	ggc Gly	gga Gly	gct Ala	gag Glu	cgg Arg 650	caa Gln	ata Ile	cgc Arg	ata Ile	gat Asp 655	cgg Arg	1	968
				Asn				ttt Phe 665						Thr		2	016
gct Ala	ggt Gly	ggc Gly 675	Leu	gga Gly	ata Ile	aat Asn	ctt Leu 680	gca Ala	acg Thr	gct Ala	gat Asp	aca Thr 685	gta Val	atc Ile	att Ile	2	064
							His	gct Ala				Ă٦a				2	112

gct Ala 705	cat His	cga Arg	ctt Leu	ggc Gly	caa Gln 710	aca Thr	aat Asn	aag Lys	gtg Val	atg Met 715	att Ile	tat Tyr	agg Arg	ctc Leu	ata Ile 720	2160
aac Asn	cga Arg	ggc Gly	acc Thr	att Ile 725	gaa Glu	gaa Glu	agg Arg	atg Met	atg Met 730	caa Gln	ttg Leu	act Thr	aaa Lys	aag Lys 735	aaa Lys	2208
atg Met	gtt Val	cta Leu	gag Glu 740	cat His	ctt Leu	gtt Val	gtt Val	ggg G1y 745	aaa Lys	ctc Leu	aaa Lys	aca Thr	caa Gln 750	aac Asn	att Ile	2256
aat Asn	cag Gln	gaa Glu 755	gag Glu	tta Leu	gat Asp	gac Asp	atc Ile 760	atc Ile	agg Arg	tat Tyr	gga Gly	tca Ser 765	aag Lys	gag Glu	ctt Leu	2304
ttt Phe	gct Ala 770	agt Ser	gaa Glu	gat Asp	gat Asp	gaa Glu 775	gca Ala	gga Gly	aag Lys	tct Ser	gga Gly 780	aaa Lys	att Ile	cat His	tat Tyr	2352
														gag Glu		2400
gag Glu	gaa Glu	gtc Val	tca Ser	gtg Val 805	gat Asp	gat Asp	gaa Glu	gag Glu	gag Glu 810	aat Asn	gga Gly	ttc Phe	tta Leu	aag Lys 815	gct Ala	2448
														gca Ala		2496
tta Leu	gag Glu	gca Ala 835	cag Gln	aga Arg	gtc Val	gct Ala	gct Ala 840	gaa Glu	agc Ser	aaa Lys	tct Ser	tca Ser 845	gca Ala	ggc Gly	aat Asn	2544
														ttt Phe		2592
ctg Leu 865	cac His	cag Gln	gct Ala	gag Glu	gag Glu 870	ctt Leu	aat Asn	gct Ala	ctt Leu	gga Gly 875	aaa Lys	agg Arg	aag Lys	aga Arg	agt Ser 880	2640
														ttg Leu 895		2688
														aca Thr		2736
ggt Gly	gaa Glu	gca Ala 915	gca Ala	gga Gly	caa Gln	gga Gly	gtt Val 920	cag Gln	acg Thr	ggt Gly	cga Arg	cgg Arg 925	ccg Pro	tac Tyr	aga Arg	2784
aga Arg	aag Lys 930	ggt Gly	cgc Arg	gat Asp	aat Asn	ttg Leu 935	gaa Glu	cca Pro	act Thr	ccg Pro	ttg Leu 940	atg Met	gaa Glu	ggt Gly	gag Glu	2832
ggg Gly 945	aga Arg	tct Ser	ttc Phe	aga Arg	gta Val 950	ctg Leu	ggt Gly	ttc Phe	aac Asn	cag Gln 955	agt Ser	caa Gln	agg Arg	gcc Ala	att Ile 960	2880
ttt Phe	gta Val	cag Gln	act Thr	ttg Leu 965	atg Met	agg Arg	tat Tyr	gga Gly	gct Ala 970	ggc Gly	aat Asn	ttt Phe	gat Asp	tgg Trp 975	aag Lys	2928
gag	ttt	gtt	cct	cgc	tta	aag	cag	aag	acc	ttt 4	gaa	gaa	ata	aat	gaa	2976

Glu Phe Val Pro Arg Leu Lys Gln Lys Thr Phe Glu Glu Ile Asn Glu 980 985 990

		3	700				90	33				991	U			
tat Tyr	Gly 1	ita d le L 195	tc t eu f	tc t he l	ttg a Leu l	ys H	ac a is 1 000	att (	gct (	gaa ( Glu (	Glu I	ta ( le / 005	gac ( Asp (	gag aat Glu Asr		3024
	cca Pro 1010	acc Thr	ttt Phe	tca Ser	gat Asp	ggt Gly 1015	gtg val	ccc Pro	aag Lys	gaa Glu	gga Gly 1020	ctt Leu	aga Arg	ata Ile		3069
gaa Glu	gat Asp 1025	gtt Val	cta Leu	gtc Val	aga Arg	att Ile 1030	gct Ala	ctt Leu	ctg Leu	ata Ile	cta Leu 1035	gtt Val	cag Gln	gag Glu		3114
aag Lys	gtg Val 1040	aaa Lys	ttt Phe	gta Val	gaa Glu	gat Asp 1045	cat His	cca Pro	ggg Gly	aaa Lys	cct Pro 1050	gtt Val	ttc Phe	ccc Pro		3159
	cgc Arg 1055	att Ile	ctt Leu	gaa Glu	aga Arg	ttc Phe 1060	ccc Pro	gga Gly	ctg Leu	aga Arg	agt Ser 1065	gga Gly	aaa Lys	att Ile		3204
	aag Lys 1070					aag Lys 1075	ata Ile	atg Met	ata Ile	cgt Arg	gct Ala 1080	gtt Val	tta Leu	aag Lys		3249
cat His	ggg Gly 1085	tac Tyr	gga Gly	cgg Arg	tgg Trp	caa Gln 1090	gct Ala	att Ile	gtt Val	gat Asp	gac Asp 1095	aaa Lys	gag Glu	ttg Leu		3294
ggg Gly	atc Ile 1100	caa Gln	gag Glu	ctt Leu	atc Ile	tgc Cys 1105	aaa Lys	gaa Glu	ttg Leu	aat Asn	ttc Phe 1110	cct Pro	cac His			3339
agt Ser	ttg Leu 1115	tct Ser	gct Ala	gct Ala	gaa Glu	caa Gln 1120	gct Ala	ggt Gly	ttg Leu	cag Gln	ggg Gly 1125	cag Gln	aat Asn			3384
agt Ser	ggg Gly 1130	ggc Gly	tct Ser	aat Asn	ccg Pro	gga Gly 1135	gca Ala	cag Gln	act Thr	aac Asn	cag Gln 1140	aat Asn	cct Pro			3429
agc Ser	gtt Val 1145	att Ile	act Thr	ggg Gly	aac Asn	aat Asn 1150	aat Asn	gct Ala	tct Ser	gct Ala	gat Asp 1155		gct Ala	caa Gln		3474
gta Val	aac Asn 1160	tcg Ser	atg Met	ttc Phe	tat Tyr	tat Tyr 1165	cgg Arg	gac Asp	atg Met	cag Gln	aga Arg 1170	cga Arg	ctt Leu	gtt Val		3519
gag Glu	ttt Phe 1175	gtg Val	aaa Lys	aag Lys	cga Arg	gtt Val 1180	ctg Leu	ctt Leu	ttg Leu	gag Glu	aag Lys 1185	gcg Ala	atg Met	aat Asn		3564
	gaa Glu 1190	tac Tyr	gca Ala	gag Glu	gaa Glu	tat Tyr 1195	tat Tyr	gga Gly	ctt Leu	ggt Gly	ggc Gly 1200		tca Ser			3609
atc Ile	cct Pro 1205	act Thr	gaa Glu	gaa Glu	cca Pro	gaa Glu 1210	gct Ala	gaa Glu	cca Pro	aag Lys	atc Ile 1215	gct Ala	gac Asp	aca Thr		3654
gtg Val	gga Gly 1220	gtg Val	agc Ser	ttt Phe	att Ile	gag Glu 1225					atg Met 1230		gat Asp			3699
	cct Pro	aag Lys	act Thr	gat Asp	cct Pro	atc Ile	act Thr	tca Ser	gaa Glu 5	Glu	att Ile	atg Met	ggg Gly	gct Ala	,	3744

	1235					1240					1245				
gct Ala	gtt Val 1250	gac Asp	aac Asn	aac Asn	caa Gln	gcg Ala 1255	cgg Arg	gtc val	gaa Glu	ata Ile	gct Ala 1260	caa Gln	cat His	tat Tyr	3789
	cag Gln 1265	atg Met	tgc Cys	aaa Lys	ctt Leu	ctt Leu 1270	gat Asp	gag Glu	aac Asn	gct Ala	cgg Arg 1275	gaa Glu	tca Ser	gtc Val	3834
caa Gln	gca Ala 1280	tat Tyr	gta Val	aac Asn	aac Asn	caa Gln 1285	cca Pro	ccg Pro	agt Ser	acc Thr	aag Lys 1290	gtg val	aat Asn		3879
	ttc Phe 1295	cgt Arg	gca Ala	ctc Leu	aaa Lys	tct Ser 1300	atc Ile	aat Asn	ggt Gly	aac Asn	att Ile 1305	aac Asn	aca Thr	atc Ile	3924
ctt Leu	tcg Ser 1310	att Ile	aca Thr	tct Ser	gat Asp	caa Gln 1315	tcc Ser	aag Lys	tca Ser	cat His	gaa Glu 1320	gac Asp	gac Asp		3969
aag Lys	cca Pro 1325	gac Asp	cta Leu	aac Asn	aat Asn	gtt Val 1330	gag Glu	atg Met	aag Lys	gac Asp	acg Thr 1335	gcc Ala	gaa Glu		4014
_	aaa Lys 1340	ccg Pro	tta Leu	aga Arg	ggt Gly	ggc Gly 1345	gtc Val	gtc Val	gat Asp	ctg Leu	aat Asn 1350	gtg Val	gtg Val	gag Glu	4059
gga Gly	gag Glu 1355	gag Glu	aac Asn	att Ile	gct Ala	gaa Glu 1360	gct Ala	agt Ser	gga Gly	agt Ser	gtt Val 1365	gat Asp	gta Val	aaa Lys	4104
	gaa Glu 1370	gaa Glu	gcc Ala	aaa Lys	gaa Glu	gaa Glu 1375	gag Glu	aag Lys	cca Pro	aag Lys	aac Asn 1380		gtc Val		4149
gat Asp	tga														4155
<210	)> 2	204													

Met Ser Ser Leu Val Glu Arg Leu Arg Ile Arg Ser Asp Arg Lys Pro 10 15

Val Tyr Asn Leu Asp Asp Ser Asp Asp Asp Asp Phe Val Pro Lys Lys 20 25 30

Asp Arg Thr Phe Glu Gln Val Glu Ala Ile Val Arg Thr Asp Ala Lys 35 40 45

Glu Asn Ala Cys Gln Ala Cys Gly Glu Ser Thr Asn Leu Val Ser Cys 50 60

Asn Thr Cys Thr Tyr Ala Phe His Ala Lys Cys Leu Val Pro Pro Leu 65 70 75 80

<sup>&</sup>lt;211> 1384 <212> PRT <213> Arabidopsis thaliana

<sup>&</sup>lt;400> 2

Lys Asp Ala Ser Val Glu Asn Trp Arg Cys Pro Glu Cys Val Ser Pro 85 90 95 Leu Asn Glu Ile Asp Lys Ile Leu Asp Cys Glu Met Arg Pro Thr Lys
100 105 110 Ser Ser Glu Gln Gly Ser Ser Asp Ala Glu Pro Lys Pro Ile Phe Val 115 120 125 Lys Gln Tyr Leu Val Lys Trp Lys Gly Leu Ser Tyr Leu His Cys Ser 130 135 140 Trp Val Pro Glu Lys Glu Phe Gln Lys Ala Tyr Lys Ser Asn His Arg 145 150 155 160 Leu Lys Thr Arg Val Asn Asn Phe His Arg Gln Met Glu Ser Phe Asn 165 170 175 Asn Ser Glu Asp Asp Phe Val Ala Ile Arg Pro Glu Trp Thr Thr Val 180 185 190 Asp Arg Ile Leu Ala Cys Arg Glu Glu Asp Gly Glu Leu Glu Tyr Leu 195 200 205 Val Lys Tyr Lys Glu Leu Ser Tyr Asp Glu Cys Tyr Trp Glu Ser Glu 210 215 220 Ser Asp Ile Ser Thr Phe Gln Asn Glu Ile Gln Arg Phe Lys Asp Val 225 230 235 240 Asn Ser Arg Thr Arg Arg Ser Lys Asp Val Asp His Lys Arg Asn Pro 245 250 255 Arg Asp Phe Gln Gln Phe Asp His Thr Pro Glu Phe Leu Lys Gly Leu 260 265 270 Leu His Pro Tyr Gln Leu Glu Gly Leu Asn Phe Leu Arg Phe Ser Trp 275 280 285 Ser Lys Gln Thr His Val Ile Leu Ala Asp Glu Met Gly Leu Gly Lys 290 295 300 Thr Ile Gln Ser Ile Ala Leu Leu Ala Ser Leu Phe Glu Glu Asn Leu 305 310 315 320 Ile Pro His Leu Val Ile Ala Pro Leu Ser Thr Leu Arg Asn Trp Glu 325 330 335 Arg Glu Phe Ala Thr Trp Ala Pro Gln Met Asn Val Val Met Tyr Phe 340 345 350

Gly Thr Ala Gln Ala Arg Ala Val Ile Arg Glu His Glu Phe Tyr Leu 355 360 365 Ser Lys Asp Gln Lys Lys Ile Lys Lys Lys Ser Gly Gln Ile Ser 370 380 Ser Glu Ser Lys Gln Lys Arg Ile Lys Phe Asp Val Leu Leu Thr Ser 385 390 395 400 Tyr Glu Met Ile Asn Leu Asp Ser Ala Val Leu Lys Pro Ile Lys Trp 405 410 415 Glu Cys Met Ile Val Asp Glu Gly His Arg Leu Lys Asn Lys Asp Ser 420 425 430 Lys Leu Phe Ser Ser Leu Thr Gln Tyr Ser Ser Asn His Arg Ile Leu 435 440 445 Leu Thr Gly Thr Pro Leu Gln Asn Asn Leu Asp Glu Leu Phe Met Leu 450 460 Met His Phe Leu Asp Ala Gly Lys Phe Gly Ser Leu Glu Glu Phe Gln 465 470 475 480 Glu Glu Phe Lys Asp Ile Asn Gln Glu Glu Gln Ile Ser Arg Leu His 485 490 495 Lys Met Leu Ala Pro His Leu Leu Arg Arg Val Lys Lys Asp Val Met 500 505 510 Lys Asp Met Pro Pro Lys Lys Glu Leu Ile Leu Arg Val Asp Leu Ser 515 520 525 Ser Leu Gln Lys Glu Tyr Tyr Lys Ala Ile Phe Thr Arg Asn Tyr Gln 530 540 Val Leu Thr Lys Lys Gly Gly Ala Gln Ile Ser Leu Asn Asn Ile Met 545 550 555 560 Met Glu Leu Arg Lys Val Cys Cys His Pro Tyr Met Leu Glu Gly Val 565 570 575 Glu Pro Val Ile His Asp Ala Asn Glu Ala Phe Lys Gln Leu Leu Glu 580 585 590 Ser Cys Gly Lys Leu Gln Leu Leu Asp Lys Met Met Val Lys Leu Lys 595 600 Glu Gln Gly His Arg Val Leu Ile Tyr Thr Gln Phe Gln His Met Leu 610 615 620 Asp Leu Leu Glu Asp Tyr Cys Thr His Lys Lys Trp Gln Tyr Glu Arg 8

Ile Asp Gly Lys Val Gly Gly Ala Glu Arg Gln Ile Arg Ile Asp Arg 645 650 655 Phe Asn Ala Lys Asn Ser Asn Lys Phe Cys Phe Leu Leu Ser Thr Arg 660 665 670 Ala Gly Gly Leu Gly Ile Asn Leu Ala Thr Ala Asp Thr Val Ile Ile 675 680 685 Tyr Asp Ser Asp Trp Asn Pro His Ala Asp Leu Gln Ala Met Ala Arg 690 695 700 Ala His Arg Leu Gly Gln Thr Asn Lys Val Met Ile Tyr Arg Leu Ile 705 710 715 720 Asn Arg Gly Thr Ile Glu Glu Arg Met Met Gln Leu Thr Lys Lys Lys 725 730 735 Met Val Leu Glu His Leu Val Val Gly Lys Leu Lys Thr Gln Asn Ile 740 745 750 Asn Gln Glu Leu Asp Asp Ile Ile Arg Tyr Gly Ser Lys Glu Leu 755 760 765 Phe Ala Ser Glu Asp Asp Glu Ala Gly Lys Ser Gly Lys Ile His Tyr 770 780 Asp Asp Ala Ala Ile Asp Lys Leu Leu Asp Arg Asp Leu Val Glu Ala 785 790 795 800 Glu Glu Val Ser Val Asp Asp Glu Glu Glu Asn Gly Phe Leu Lys Ala 805 810 Phe Lys Val Ala Asn Phe Glu Tyr Ile Asp Glu Asn Glu Ala Ala 820 825 830 Leu Glu Ala Gln Arg Val Ala Ala Glu Ser Lys Ser Ser Ala Gly Asn 835 840 845 Ser Asp Arg Ala Ser Tyr Trp Glu Glu Leu Leu Lys Asp Lys Phe Glu 850 860 Leu His Gln Ala Glu Glu Leu Asn Ala Leu Gly Lys Arg Lys Arg Ser 865 870 875 880 Arg Lys Gln Leu Val Ser Ile Glu Glu Asp Asp Leu Ala Gly Leu Glu 885 890 895 Asp Val Ser Ser Asp Gly Asp Glu Ser Tyr Glu Ala Glu Ser Thr Asp 900 905 910

Gly Glu Ala Ala Gly Gln Gly Val Gln Thr Gly Arg Arg Pro Tyr Arg 915 920 925

Arg Lys Gly Arg Asp Asn Leu Glu Pro Thr Pro Leu Met Glu Gly Glu 930 940

Gly Arg Ser Phe Arg Val Leu Gly Phe Asn Gln Ser Gln Arg Ala Ile 945 950 955 960

Phe Val Gln Thr Leu Met Arg Tyr Gly Ala Gly Asn Phe Asp Trp Lys 965 970 975

Glu Phe Val Pro Arg Leu Lys Gln Lys Thr Phe Glu Glu Ile Asn Glu 980 985 990

Tyr Gly Ile Leu Phe Leu Lys His Ile Ala Glu Glu Ile Asp Glu Asn 995 1000 1005

Ser Pro Thr Phe Ser Asp Gly Val Pro Lys Glu Gly Leu Arg Ile 1010 1015 1020

Glu Asp Val Leu Val Arg Ile Ala Leu Leu Ile Leu Val Gln Glu 1025 1030 1035

Lys Val Lys Phe Val Glu Asp His Pro Gly Lys Pro Val Phe Pro 1040 1045 1050

Ser Arg Ile Leu Glu Arg Phe Pro Gly Leu Arg Ser Gly Lys Ile 1055 1060 1065

Trp Lys Glu Glu His Asp Lys Ile Met Ile Arg Ala Val Leu Lys 1070 1080

His Gly Tyr Gly Arg Trp Gln Ala Ile Val Asp Asp Lys Glu Leu 1085 1090 1095

Gly Ile Gln Glu Leu Ile Cys Lys Glu Leu Asn Phe Pro His Ile 1100 1105 1110

Ser Leu Ser Ala Ala Glu Gln Ala Gly Leu Gln Gly Gln Asn Gly 1115 1120 1125

Ser Gly Gly Ser Asn Pro Gly Ala Gln Thr Asn Gln Asn Pro Gly 1130 1140

Ser Val Ile Thr Gly Asn Asn Asn Ala Ser Ala Asp Gly Ala Gln 1145 1150 1155

Val Asn Ser Met Phe Tyr Tyr Arg Asp Met Gln Arg Arg Leu Val 1160 1165 1170 Glu Phe Val Lys Lys Arg Val Leu Leu Glu Lys Ala Met Asn 1175 1180 1185

Tyr Glu Tyr Ala Glu Glu Tyr Tyr Gly Leu Gly Gly Ser Ser Ser 1190 1195 1200

Ile Pro Thr Glu Glu Pro Glu Ala Glu Pro Lys Ile Ala Asp Thr 1205 1210 1215

Val Gly Val Ser Phe Ile Glu Val Asp Asp Glu Met Leu Asp Gly 1220 1230

Leu Pro Lys Thr Asp Pro Ile Thr Ser Glu Glu Ile Met Gly Ala 1235 1240 1245

Ala Val Asp Asn Asn Gln Ala Arg Val Glu Ile Ala Gln His Tyr 1250 1260

Asn Gln Met Cys Lys Leu Leu Asp Glu Asn Ala Arg Glu Ser Val 1265 1270 1275

Gln Ala Tyr Val Asn Asn Gln Pro Pro Ser Thr Lys Val Asn Glu 1280 1285 1290

Ser Phe Arg Ala Leu Lys Ser Ile Asn Gly Asn Ile Asn Thr Ile 1295 1300 1305

Leu Ser Ile Thr Ser Asp Gln Ser Lys Ser His Glu Asp Asp Thr 1310 1320

Lys Pro Asp Leu Asn Asn Val Glu Met Lys Asp Thr Ala Glu Glu 1325 1330 1335

Thr Lys Pro Leu Arg Gly Gly Val Val Asp Leu Asn Val Val Glu 1340 1345 1350

Gly Glu Glu Asn Ile Ala Glu Ala Ser Gly Ser Val Asp Val Lys 1355 1360 1365

Met Glu Glu Ala Lys Glu Glu Lys Pro Lys Asn Met Val Val 1370 1380

Asp

<210> 3 <211> 9353

<212> DNA

<213> Arabidopsis thaliana

<400> 3 atgagtagtt tggtggagag gcttcgcata cgatctgata ggaaaccagt ttataaccta

	•					
gatgattctg	atgatgacga	cttcgttcct	aaaaaagatc	gaacctttga	gcaagtcgag	120
gctattgtca	gaactgatgc	ggtttgtttc	tcctctcgag	cttattgttc	agcttttact	180
gttttatgtg	ttctatttta	atccttttt	ttgtgttgtt	actctgaatt	tgtagaaaga	240
aaatgcatgt	caggcttgtg	gggaaagtac	taatcttgta	agctgcaata	catgcactta	300
tgcgttccat	gctaaatgct	tagttccacc	tcttaaagat	gcttccgtgg	aaaattggag	360
atgccctgaa	tgtgtaagat	tttagttacg	gtccacaatt	atgttttggg	atgctacagg	420
ttccattttt	cttacatgga	agaattgttg	tttacatttg	caggttagtc	ctcttaacga	480
gatagataag	atattggatt	gtgaaatgcg	tcctacaaaa	tctagtgaac	aaggttcctc	540
cgatgcggaa	ccgaagccaa	tttttgtgaa	acagtatctc	gtgaagtgga	agggattatc	600
ataccttcac	tgctcttggt	agttactgcg	tgtcttttt	gctgtctgga	cacgctaatt	660
atcaatgttt	ctttctgtga	acactataat	atgtgattta	tttcctttta	ctaatcatag	720
ggtgcctgag	aaggagttcc	agaaggctta	taagtcaaat	catcgtttaa	aaaccagagt	780
gaacaatttt	caccgtcaaa	tggagtcatt	caataacagc	gaagatgatt	ttgttgccat	840
acgtcctgag	tggaccactg	ttgatcggat	tcttgcctgc	aggtctagag	aatggaatta	900
attcctttat	ttatctatct	gccaactttt	tttttaatat	ccttgttttc	agcataatcc	960
attctctaat	aaacacgtat	ctttgataga	gtgctgctta	acctaaattt	actgttatca	1020
cgattttggg	tctctgaaac	atgataaatg	acctgcttac	ctttttttc	ttctttttaa	1080
gttaccattt	tcttagttgt	ttcgtaaatc	aggaattgtg	acagttgcat	tggtttcttt	1140
tatgatatag	agaggaagat	ggggagctgg	aatatcttgt	caaatataaa	gagctatcct	1200
atgatgaatg	ttattgggag	tcagaatcag	acatctcaac	cttccagaat	gaaattcaaa	1260
ggttcaagga	tgtaaattct	agaactcgca	gaagtaaaga	tgttgaccat	aaaagaaatc	1320
ccagagactt	tcaacagttt	gatcatactc	ctgaattcct	caaaggtatt	tggatcacct	1380
taaatcatat	actataaatg	tttcttatat	ttggtactta	tagatgttat	gatttatttg	1440
tttcctgcga	ttgaaggctt	gttacatcca	taccagcttg	agggacttaa	ttttttgcgg	1500
ttctcgtggt	caaaacagac	gcatgtaatc	cttgctgatg	aaatgggact	aggtaatttt	1560
tcaattgtcc	cacttgggtg	gtcacataga	tcttttcatc	cattgtaagg	ggcctttgtt	1620
ttctattcct	gtaatgttgt	gagattttc	ctgttacagg	caagacaatt	caaagcattg	1680
cccttttagc	ttcacttttt	gaggagaacc	tcattccgca	tttggtaatt	gctcctctat	1740
cgactctgcg	taactgggag	agagagtttg	ccacatgggc	cccacagatg	aacgtggtat	1800
gtatgcagtt	atacacgcaa	tgatctgtgc	catttgtatg	tttttgttgt	ttgttaatgg	1860
aatggtcttc	gtggtcattt	gacgggtagg	ttatgtattt	tggcactgcg	caagctcgag	1920
cagttatcag	agaacatgag	ttttacttat	cgaaagatca	aaaaaagatc	aagaaaaaga	1980
aatctggaca	aataagtagc	gaaagcaagc	aaaaaagaat	caagtttgat	gtcctcctca	2040
catcgtatga	gatgatcaac	ctagattcag	cagttctaaa	accaattaag	tgggagtgca	2100
tggtaactct	tattctctaa	tgagacttta	ctttctctta 12	gtcgtctctc	tttctctctt	2160
			12			

acatgttgcc tagtaacaat tgttttgggc agattgttga tgaaggtcat cgactgaaaa 2220 2280 ataaggattc aaagctgttc tcttcattga cacagtattc aagtaaccac cgtattcttc tgacaggaac accacttcag gttcgtcatt tgagtttgat ttctgaagtt tatactttca 2340 2400 atagttgtat ctgagcatag tagctacgat ttgcaatgag aattgttata tattatcttg cactaatgtc ttacctgatt agttgcaata tgttactgat gattatgtgg tgcctttaca 2460 2520 gaacaacttg gatgaacttt tcatgctcat gcattttctt gatgcgggga aggtatcaca 2580 agaatagcaa agataaataa gttcgcatac ttaacagaat tttatgtagc taacatgtta tttgattgca caatacttgc agtttggaag tttggaggag ttccaggagg agttcaaaga 2640 tattaatcaa gaggagcaga tctcaaggtt gcacaaaatg ttggctccac atttgctcag 2700 2760 aagtattaac caaaactatt tgttcatctt ttttaattta tatgtgtttc aaaagtttgg 2820 ttggagggaa tctttcatag taataatttt atgatcttaa ccatgctgtc tcgtattttg attgctcttc caggggtaaa aaaagacgta atgaaagaca tgccccccaa aaaggagctc 2880 2940 attttgcgtg ttgatctgag cagtctgcag aaagaatatt acaaagctat ttttacccgt 3000 aattatcaag tattgacaaa aaagggaggt gctcaagtaa gttcttttta atttttgttt 3060 acactttttg gatcattaaa cctcataggt ggggtagaaa ccaggtcaac tgtaatcgtc tagtgaatgt attggtctat ttctgtttca gatttccctt aataacatta tgatggaatt 3120 acgaaaagta tgctgccatc cttatatgct agagggtgtt gagccagtta ttcacgacgc 3180 aaatgaagct ttcaagtaat atctcatttc ccaaaaatgg ttatctgttt attactactt 3240 3300 attaaagtcg tctgctaact tttgcgttga acgttttctt atatgtatca aagacaactt ttggagtctt gtggaaagct gcaacttcta gataaaatga tggtcaaact gaaagagcaa 3360 3420 ggacacagag tcctaatata cacacagttt cagcatatgc tggacttact tgaagactac tgtacccata aggtatttga acttcttata tgtacagtct gtttcagtag attttcattc 3480 ttgttgtttt tgtagaatat cattttgaca ctgtagaatc aactctacca ttttctagtg 3540 ttagagtact taggcacaat tatggaaata caagcatgtg ctgaaattga gagtatatga 3600 gcattctgtg cccaactgaa agagcaaaga cacaaagttt ccttataaac acagtacaaa 3660 tcacaagttt agccatcttc tatgtacagt agttttccaa taggtcgagc atgtgctgaa 3720 actgtgtgta cagagttctc ataaacacac agtttcagca tatgctggat ctacttgaag 3780 actactgttc ttataaggta ctgaacttgt tatctgtact gcgtatatac gagatctctg 3840 tattcttgct cttttatttt gacactttgt tctcatatac actcggttca gcacatgctc 3900 gacttactgc ctaaggatct tgaaaaaggt agagttgatt ctatgtctag gtgcaattac 3960 tttcttagaa tttttgtcat tacttactct gttggcaata taacttcttt attccctcaa 4020 agattacttt ttttggtttc ttgaaatgcc attatcaata ccattgcttt tgctgacgca 4080 tgcacttgag acaacttgtt tttatctctt tctagcacat ttttttttaa catgcagtta 4140 aggaaaattc tcatatgatt tacgctgttc attttcttgt ctttgtcaga aatggcagta 4200

cgagcgaatt	gatggaaagg	ttggcggagc	tgagcggcaa	atacgcatag	atcggttcaa	4260
tgccaaaaat	tctaacaagt	tttgttttt	gctctccaca	agagctggtg	gcttaggaat	4320
aaatcttgca	acggctgata	cagtaatcat	ttatgacagg	tttgaatttc	agcttctctt	4380
agtgtcatct	gtactcttt	catagttatt	gtgtcaagct	gtaagaggaa	ctatttggct	4440
tgatagcata	atattttgga	agtttaatgt	tgatttttaa	gtgaattggg	ttgtgatgag	4500
tgataaaaag	gcacttggct	tttttccaat	aacagctatt	tcttgaacat	ggatgttcta	4560
agacagcagg	aagatcagga	aaattattaa	ccgctatctt	gctaataatt	agattttgta	4620
ggcatgcaat	atgggtggcg	tccatgggat	cctgcttgga	tggcagtttg	ttttggttta	4680
cgcctgttca	cattttcata	cgtacgattg	aaactgtttt	atctgtttct	gtagtgactg	4740
gaatcctcat	gctgatcttc	aagcaatggc	tagagctcat	cgacttggcc	aaacaaataa	4800
ggttttaaat	tttatctctt	agtgctgtca	acttgcaatt	ttgtgttctt	ttttgtagtt	4860
tccctaattt	tccttatatt	ttcctttagg	tgatgattta	taggctcata	aaccgaggca	4920
ccattgaaga	aaggatgatg	caattgacta	aaaagaaaat	ggttctagag	catcttgttg	4980
ttgggaaact	caaaacacaa	aacattaatc	aggtaaactt	ttattgcttg	aagccttttt	5040
acttgattac	aaatttctca	acggattgga	gctggaaggt	agaaattcca	agaagaacac	5100
cttcggttat	aacttataag	tgtgaaatta	aaagataaaa	actttagaga	gaaggggtcc	5160
atatttgtta	attgtttgtc	actaagtatg	tgtttgtttt	gttttcctga	ctgcaattta	5220
ggaagagtta	gatgacatca	tcaggtatgg	atcaaaggag	ctttttgcta	gtgaagatga	5280
tgaagcagga	aagtctggaa	aaattcatta	tgatgatgcg	gctatagaca	agtaatagac	5340
tccttactct	tttcctcttg	ttttgtttt	gattaacaag	gatatctgat	ctttccgatt	5400
gctcctttct	tatgaaagct	tttgcagtca	attgcatggg	cgtatttcat	tatttgtctc	5460
tatcttctgt	tctgcagatt	gcttgatcgt	gatctcgtgg	aggcagagga	agtctcagtg	5520
gatgatgaag	aggagaatgg	attcttaaag	gctttcaagg	ttttcttgcc	tcttactatt	5580
cttcctcttc	tattagtttt	ctctgaatca	gtgtttactg	atttcaatgc	tccattggag	5640
tctatgctta	attgtattct	tatattccat	gatattcaga	ctgtggttgg	ctatcgaaat	5700
cccttctgct	gtgcacaatc	ttgtcaaatc	attacgtgct	aagtttgtag	gatcaataca	5760
ctttatgcca	gttcgctttg	atgcttatag	acagtcttta	gaaagtgtct	attgattgtt	5820
cgttccggct	caatgtgaaa	gccaacttaa	tgaaaattag	tgatgatgac	ttaagttaga	5880
aatttatgct	tgtggtgatg	ttgattgagc	caatttattg	atttggttat	atttcttttg	5940
aaccctgatc	atattgaatg	cgttatatga	gtggtcttta	gacttagctg	gaacataagg	6000
ctgtgtcctg	cattgctgct	tgtcacctct	taatattcga	actccctaaa	acattgtttg	6060
tctttgtgtg	catatagaac	tgttctgaag	caaatagggt	gtctggtact	gtttagtgtc	6120
attaactctg	aaaatgattt	cccttgtaag	attctgtgat	cttcctgtat <sup>.</sup>	tgtaggtggc	6180
taattttgaa	tatatagatg	aaaatgaggc	agcagcatta	gaggcacaga	gagtcgctgc	6240
tgaaagcaaa	tcttcagcag	gcaattctga	tagagcaagt 14	tattgggaag	agttgttaaa	6300
			<b>-</b> •			

agataaattt gagctgcacc aggctgagga gcttaatgct cttggaaaaa ggaagagaag 6360 6420 tcgcaagcag gtttggtctc ttcttgatcc cccttatcca attgtggcat catattgata 6480 actggatttt tcaccattta tgttctttct gattctgtcc tgtttcatat atttattcat 6540 gttgtctaac ttttcctttt gaattcctta ggtagctaaa ttcagaaagt aataatttag ttgactgtat ccttctaaat tgagaaagta taatttagtt gactgtatcc agtataaaac 6600 6660 taaacgccct tgtcctccta tcaactggtt tgacagatct tatgggttta catgttggat caagtaattg gggttggtag aggctcaatt aactatagtc ttctgttttc ctctgcaaga 6720 aatacgtttt gtttcactct ctaacttgat atagctcaat tactgacaat atacattggt 6780 ttggtctgcc atcatcgttt catgtctttc aataaaggct gttctaattc ttctatggga 6840 6900 tttttttcat agttggtatc cattgaagaa gatgatcttg ctggtttgga agatgtgagc tctgatggag atgaaagtta tgaagctgag tcaacagatg gtgaagcagc aggacaagga 6960 7020 gttcagacgg gtcgacggcc gtacagaaga aagggtcgcg gtattaccac gtttcggatt taatttaatt tgtaatggag ctgaaaatga ctgatattag aagtgtgcgc agtttattag 7080 atgagttttt tttctataga taatttggaa ccaactccgt tgatggaagg tgaggggaga 7140 7200 tctttcagag tactgggttt caaccagagt caaagggcca tttttgtaca gactttgatg aggtatctac tttccattaa ggcctttaga cgccagaagc tattctgtct aaattttaca 7260 gtttcatccc ccgatgcatc taaattatca tcagtcttgt ggtgctcaat atttacaagt 7320 ttttccggtt ggacaaaata attgcaggta tggagctggc aattttgatt ggaaggagtt 7380 tgttcctcgc ttaaagcaga agacctttga agaaataaat gagtacgggc tcaacccttt 7440 aatgctcttc tcttctgctt ctttacaaaa aacgcatcat tataaaaagg ctttctggtt 7500 tattctttaa ctaatttttt aatgactgtt tctcagatat ggaatactct tcttgaagca 7560 CattgCtgaa gaaatagacg agaattctcc aaccttttca ggtgatcgat aattgatatt 7620 ttcactgttt gctgcttttc cctaaatgag atcattgctt ctcctgttaa ccggttaaat 7680 7740 gatgttctag tcagaattgc tcttctgata ctagttcagg agaaggtgag tctattgact 7800 ttaattcttc attaagttct ctcttttata tctgagtttt tttttggtat atgttacttc 7860 tagtctatag tttagctctg tacataagtt tttaatacag taatgtatgt tcaaacctca 7920 ctaagatttg gatcccgggt tacttatgtt tttttggtgc tctggcccga caggtgaaat 7980 ttgtagaaga tcatccaggg aaacctgttt tcccctctcg cattcttgaa agattccccg 8040 gactgagaag tggaaaaatt tggaaggagg aacatgacaa gataatgata cgtgctgttt 8100 taaagtatga accctgcacc actgttctta ccgaatggtt ttattttctc atcattctcc 8160 attacttgct cacattttct tttccttctc tggaaatttg aatctttagg catgggtacg 8220 gacggtggca agctattgtt gatgacaaag agttggggat ccaagagctt atctgcaaag 8280 aattgaattt ccctcacata agtttgtctg ctgctgaaca agctggtttg caggggcaga 8340

atggtagtgg gggctctaat	ccgggagcac	agactaacca	gaatcctgga	agcgttatta	8400
ctgggaacaa taatgcttct	gctgatgggg	ctcaagtaaa	ctcgatgttc	tattatcggg	8460
acatgcagag acgacttgtt	gagtttgtga	aaaagcgagt	tctgcttttg	gagaaggcga	8520
tgaattatga atacgcagag	gaatattatg	tatgttgtac	catctgcagt	gttggtactt	8580
actcacatgt tttgcgctga	attgtttaac	tttgattgaa	tctctggttg	cagggacttg	8640
gtggctcatc atctatccct	actgaagaac	cagaagctga	accaaagatc	gctgacacag	8700
tgggagtgag ctttattgag	gttgatgatg	aaatgcttga	tggacttcct	aagactgatc	8760
ctatcagtaa gttccatcac	aagtttcttt	atttaacgag	ttgttgattc	taatgtgagc	8820
tctctgaatc tcgctgcagc	ttcagaagaa	attatggggg	ctgctgttga	caacaaccaa	8880
gcgcgggtcg aaatagctca	acattataac	caggtaagct	atgcttttt	cctttggtgg	8940
taggctaatg tctagaacta	gtatatcaca	ctaatatctc	tccggttatt	cagatgtgca	9000
aacttcttga tgagaacgct	cgggaatcag	tccaagcata	tgtaaacaac	caaccaccga	9060
gtaccaaggt gaatgagagc	ttccgtgcac	tcaaatctat	caatggtaac	attaacacaa	9120
tcctttcgat tacatctgat	caatccaagt	cacatgaaga	cgacaccaag	ccagacctaa	9180
acaatgttga gatgaaggac	acggccgaag	aaacaaaacc	gttaagaggt	ggcgtcgtcg	9240
atctgaatgt ggtggaggga	gaggagaaca	ttgctgaagc	tagtggaagt	gttgatgtaa	9300
aaatggaaga agccaaagaa	gaagagaagc	caaagaacat	ggtcgttgat	tga	9353

<211> 1403 <212> DNA

<213> Arabidopsis thaliana

<400> 4 atgaacctta aggagacgga gctttgtctt ggcctccccg gaggcactga aaccgttgaa 60 agtccggcca agtcgggtgt tgggaacaag agaggcttct ccgagaccgt tgatctcaaa 120 cttaatcttc aatctaacaa acaaggacat gtggatctca acactaatgg agctcccaag 180 gagaagacct tccttaaaga cccttctaag cctcctgcta agtaagttct atttacacaa 240 ttccttaaga agaagacctt ccttaaaagg gaagactttt tttttttt tttgagataa 300 aaagactaat agttgatata aaagttctta aaatacatat atatgaaaga tgtaaggatg 360 cataagtaat aacgttattg aatgtgtgtg tgtgttgtta tattctatgc agagcacaag 420 tggtgggttg gccatcggtg aggaactacc ggaaaaatgt tatggctaat cagaagagcg 480 gcgaagcaga ggaggcaatg agtagtggtg gaggaaccgt cgcctttgtg aaggtttcca 540 tggatggagc tccttatctt cggaaggttg acctcaagat gtacaccagc tacaaggatc 600 tctctgatgc cttggccaaa atgttcagct cctttaccat gggtatgcat tttcagacat 660 ataagtcgaa ttatcattat tatttttgtg tttacttaca attttttctt tttaacgata 720 780 gagttatgga gcacaaggga tgatagattt catgaacgag agtaaagtga tggatctgtt 840

gaacag	ttct gagtatgttc caag	ctacga gga	acaaagat	ggtgactgga	tgctcgttgg	900
tgatgt	cccc tggccgtgag tttc	ctcatt cti	tcttgctt	tcattattat	gaccaaaatt	960
attctc	taaa caaaaaaaac aata	ittctct aaa	agcattat	tattgatatt	acttatcaaa	1020
aaaata	caca aaatgataat caat	atccat gto	gttataaa	cacgcacagc	catcttttgg	1080
ttggca	tggg acagaactca gaga	icagaga aga	atgtttat	atataaatac	taactcatca	1140
atatgt	tacc tcatttgtag ctgg	cacata tto	ctttcact	ttcaatagat	ttctaaattt	1200
agtcac	caac ccaaatcccg attt	caggat gt1	ttgtcgag	tcatgcaaac	gtttgcgcat	1260
aatgaa	agga tccgaagcaa ttgg	acttgg taa	agttttct	tttctgttcg	tttctataag	1320
tggctc	tttt ctgtttttcc aata	atgctc gtg	gtttttt	ttcagctcca	agagcaatgg	1380
agaagt	tcaa gaacagatca tga					1403
<210> <211> <212> <213>	5 21 DNA Artificial Sequence					
<220> <223>	synthetic oligonucl	eotide				
<400> catatte	5 ctga tttaagacat a					21
<210> <211> <212> <213>	6 21 DNA Artificial Sequence	<b>.</b>				
<220> <223>	synthetic oligonucl	eotide				
<400> aatcaa	6 tgca tattgtcctc t					21
<210> <211> <212> <213>	7 21 DNA Artificial Sequence					
<220> <223>	synthetic oligonucl	eotide				
<400> ttatgg	7 ctaa tcagaagagc g					21
<210> <211> <212> <213>	8 21 DNA Artificial Sequence	<b>:</b>				
<220> <223>	synthetic oligonucl	eotide				
<400> tattcte	8 ctaa acaaaaaaaa c					21

<210> <211> <212> <213>	DNA	
<220> <223>	synthetic oligonucleotide	
<400> aattcg	9 actt ctgggtactc a	21
<210> <211> <212> <213>	DNA	
<220> <223>	synthetic oligonucleotide	
<400> aaatta	10 agtc cctcaagctg g	21
<210> <211> <212> <213>		
<220> <223>	synthetic oligonucleotide	
<400> actctg	11 aatt tgtagaaaga a	21
<210> <211> <212> <213>	12 21 DNA Artificial Sequence	
<220> <223>	synthetic oligonucleotide	
<400> gaagat	12 gatt ttgttgccat a	21
<210> <211> <212> <213>	13 21 DNA Artificial Sequence	
<220> <223>	synthetic oligonucleotide	
<400> aagatg	13 ggga gctggaatat c	21
<210> <211> <212> <213>	14 21 DNA Artificial Sequence	
<220> <223>	synthetic oligonucleotide	
.400	14	

ggctca	acac cctctagcat a	21
<210> <211> <212> <213>		
<220> <223>	synthetic oligonucleotide	
<400> catcca	15 tacc agcttgaggg a	21
<210> <211> <212> <213>	16 21 DNA Artificial Sequence	
<220> <223>	synthetic oligonucleotide	
<400> caagtt	16 tgat gtcctcctca c	21
<210> <211> <212> <213>	17 21 DNA Artificial Sequence	
<220> <223>	synthetic oligonucleotide	
<400> acatgc	17 cccc caaaaaggag c	21
<210> <211> <212> <213>	18 21 DNA Artificial Sequence	
<220> <223>	synthetic oligonucleotide	
<400> ccatca	18 attc gctcgtactg c	21
<210> <211> <212> <213>	19 21 DNA Artificial Sequence	
<220> <223>	synthetic oligonucleotide	
<400> atgtgc	19 tgaa actgtgtgta c	21
<210> <211> <212> <213>	20 21 DNA Artificial Sequence	
<220>		

<223>	synthetic oligonucleotide	
<400> ccattg	20 cttt tgctgacgca t	21
<210> <211> <212> <213>	21 21 DNA Artificial Sequence	
<220> <223>	synthetic oligonucleotide	
<400> ttcgat	21 agcc aaccacagtc t	21
<210> <211> <212> <213>	22 21 DNA Artificial Sequence	
<220> <223>	synthetic oligonucleotide	
<400> ggcatg	22 caat atgggtggcg t	21
<210> <211> <212> <213>	23 21 DNA Artificial Sequence	
<220> <223>	synthetic oligonucleotide	
<400> tcaggt	23 atgg atcaaaggag c	21
<210> <211> <212> <213>	24 21 DNA Artificial Sequence	
<220> <223>	synthetic oligonucleotide	
<400> ctcccc	24 tcac cttccatcaa c	21
<210> <211> <212> <213>	25 21 DNA Artificial Sequence	
<220> <223>	synthetic oligonucleotide	
<400> gtgcac	25 aatc ttgtcaaatc a	21
<210> <211> <212>	26 21 DNA	

<213>	Artificial Sequence	
<220> <223>	synthetic oligonucleotide	
<400> gaggca	26 acaga gagtcgctgc t	21
<210> <211> <212> <213>		
<220> <223>	synthetic oligonucleotide	
<400> tataca	27 attgg tttggtctgc c	21
<210> <211> <212> <213>	21	
<220> <223>	synthetic oligonucleotide	
<400> 28 gtagggatag atgatgagcc a 21		
<210> <211> <212> <213>	21 DNA	
<220> <223>	synthetic oligonucleotide	
<400> ccccga	29 Itgca tctaaattat c	21
	30 21 DNA Artificial Sequence	
<220> <223>	synthetic oligonucleotide	
<400> actagt	30 tcag gagaaggtga g	21
<210> <211> <212> <213>	31 21 DNA Artificial Sequence	
<220> <223>	synthetic oligonucleotide	
<400> acatgo	31 agag acgacttgtt g	21

```
<210> 32
<211> 21
<212> DNA
<213> Artificial Sequence
<220>
<223> synthetic oligonucleotide
<400> 32
cggacttcat cgaacctatt c
```